

P023P01.ST25.txt
SEQUENCE LISTING

<110> Japan Science and Technology Corporation
Kuroda, Shunichi
Tanizawa, Katsuyuki
Kondo, Akihiko
Ueda, Masakazu
Seno, Masaharu
Tada, Hiroko

<120> DRUG CONTAINING HOLLOW PROTEIN NANOPARTICLES OF PARTICLE-FORMING
PROTEIN, FUSED WITH DISEASE-TREATING TARGET-CELL-SUBSTANCE

<130> P023P01/US

<140> US 10/509,247
<141> 2004-09-28

<150> PCT/JP03/02602
<151> 2003-03-05

<150> JP2002-97280
<151> 2002-03-29

<160> 20

<170> PatentIn version 3.3

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 Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg Asp Ser His
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Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser
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Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser
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Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp
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Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
515 520 525

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
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Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
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agg Arg	agg Arg	tac Tyr	ttc Phe	cag Gln	gga Gly	atc Ile 545	cgt Arg	gtc Val	tac Tyr	ctg Leu	aaa Lys 550	gag Glu	aag Lys	aaa Lys	tac Tyr	1684
agc Ser 555	gac Asp	tgt Cys	gcc Ala	tgg Trp	gaa Glu 560	gtt Val	gtc Val	aga Arg	atg Met	gaa Glu 565	atc Ile	atg Met	aaa Lys	tcc Ser	ttg Leu 570	1732

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ttc tta tca aca aac atg caa gaa aga ctg aga agt aaa gat aga gac 1780
Phe Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp
575 580 585

ctg ggc tca tct tga gcggccgc 1803
Leu Gly Ser Ser
590

<210> 16
<211> 590
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16

Met Arg Ser Leu Leu Ile Leu Val Leu Cys Phe Leu Pro Leu Ala Ala
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Leu Gly Lys Val Arg Gln Gly Met Gly Thr Asn Leu Ser Val Pro Asn
20 25 30

Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala
35 40 45

Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp Gln Trp
50 55 60

Pro Glu Ala Asn Gln Val Gly Ala Gly Ala Phe Gly Pro Gly Phe Thr
65 70 75 80

Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln Ala Gln Gly Ile
85 90 95

Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser Thr Asn Arg Gln
100 105 110

Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg Asp Ser His
115 120 125

Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu
130 135 140

Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser
145 150 155 160

Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Gly Asp
165 170 175

P023P01.ST25.txt

Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu
180 185 190

Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile
195 200 205

Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
210 215 220

Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His
225 230 235 240

Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys
245 250 255

Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile
260 265 270

Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro
275 280 285

Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys
290 295 300

Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr
305 310 315 320

Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp
325 330 335

Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp
340 345 350

Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro
355 360 365

Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser
370 375 380

Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe
385 390 395 400

Cys Leu Trp Val Tyr Ile Asp Tyr Lys Asp Asp Asp Asp Lys Ile Pro
405 410 415

Val Gly Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser Arg Asn Thr
420 425 430

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Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro Phe Leu Cys Leu
435 440 445

Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu Met Val Lys Gly Ser
450 455 460

Gln Leu Gln Lys Ala His Val Met Ser Val Leu His Glu Met Leu Gln
465 470 475 480

Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser Ser Ala Ala Trp Asn
485 490 495

Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu His Gln Gln Leu Gln
500 505 510

His Leu Glu Thr Cys Leu Leu Gln Val Val Gly Glu Gly Glu Ser Ala
515 520 525

Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg Arg Tyr Phe Gln Gly
530 535 540

Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala Trp Glu
545 550 555 560

Val Val Arg Met Glu Ile Met Lys Ser Leu Phe Leu Ser Thr Asn Met
565 570 575

Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu Gly Ser Ser
580 585 590

<210> 17
<211> 1779
<212> DNA
<213> Artificial Sequence

<220>
<223> IFNfA gene fused with HBsAg L protein

<220>
<221> CDS
<222> (23)..(1771)
<223> IFNfA gene fused with HBsAg L protein gene

<400> 17
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1 5 10

ttc ttg cca ttg gct gct ttg ggt aag gtt cga caa ggc atg ggg acg 100
Phe Leu Pro Leu Ala Ala Leu Gly Lys Val Arg Gln Gly Met Gly Thr
15 20 25

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aat ctt tct gtt ccc aat cct ctg gga ttc ttt ccc gat cac cag ttg Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu 30 35 40	148
gac cct gcg ttc gga gcc aac tca aac aat cca gat tgg gac ttc aac Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn 45 50 55	196
ccc aac aag gat caa tgg cca gag gca aat cag gta gga gcg gga gca Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Ala 60 65 70	244
ttc ggg cca ggg ttc acc cca cca cac ggc ggt ctt ttg ggg tgg agc Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser 75 80 85 90	292
cct cag gct cag ggc ata ttg aca aca gtg cca gca gca cct cct cct Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro 95 100 105	340
gcc tcc acc aat cgg cag tca gga aga cag cct act ccc atc tct cca Ala Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro 110 115 120	388
cct cta aga gac agt cat cct cag gcc atg cag tgg aat tcc aca aca Pro Leu Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr 125 130 135	436
ttc cac caa gct ctg cta gat ccc aga gtg agg ggc cta tat ttt cct Phe His Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro 140 145 150	484
gct ggt ggc tcc agt tcc gga aca gta aac cct gtt ccg act act gcc Ala Gly Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala 155 160 165 170	532
tca ccc ata tct ggg gac cct gca ccg aac atg gag aac aca aca tca Ser Pro Ile Ser Gly Asp Pro Ala Pro Asn Met Glu Asn Thr Thr Ser 175 180 185	580
gga ttc cta gga ccc ctg ctc gtg tta cag gcg ggg ttt ttc ttg ttg Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu 190 195 200	628
aca aga atc ctc aca ata cca cag agt cta gac tcg tgg tgg act tct Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser 205 210 215	676
ctc aat ttt cta ggg gga gca ccc acg tgt cct ggc caa aat tcg cag Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln 220 225 230	724
tcc cca acc tcc aat cac tca cca acc tct tgt cct cca att tgt cct Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro 235 240 245 250	772
ggc tat cgc tgg atg tgt ctg cgg cgt ttt atc ata ttc ctc ttc atc Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile 255 260 265	820
ctg ctg cta tgc ctc atc ttc ttg ttg gtt ctt ctg gac tac caa ggt Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly 265 270 275 280	868

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270										275					280					
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		285					290					295								
ggg	cca	tgc	aag	acc	tgc	acg	att	cct	gct	caa	gga	acc	tct	atg	ttt	964				
Gly	Pro	Cys	Lys	Thr	Cys	Thr	Ile	Pro	Ala	Gln	Gly	Thr	Ser	Met	Phe					
	300					305					310									
ccc	tct	tgt	tgc	tgt	aca	aaa	cct	tcg	gac	gga	aac	tgc	act	tgt	att	1012				
Pro	Ser	Cys	Cys	Cys	Thr	Lys	Pro	Ser	Asp	Gly	Asn	Cys	Thr	Cys	Ile					
315					320					325					330					
ccc	atc	cca	tca	tcc	tgg	gct	ttc	gca	aga	ttc	cta	tgg	gag	tgg	gcc	1060				
Pro	Ile	Pro	Ser	Ser	Trp	Ala	Phe	Ala	Arg	Phe	Leu	Trp	Glu	Trp	Ala					
				335					340					345						
tca	gtc	cgt	ttc	tcc	tgg	ctc	agt	tta	cta	gtg	cca	ttt	gtt	cag	tgg	1108				
Ser	Val	Arg	Phe	Ser	Trp	Leu	Ser	Leu	Leu	Val	Pro	Phe	Val	Gln	Trp					
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ttc	gta	ggg	ctt	tcc	ccc	act	gtt	tgg	ctt	tca	gtt	ata	tgg	atg	atg	1156				
Phe	Val	Gly	Leu	Ser	Pro	Thr	Val	Trp	Leu	Ser	Val	Ile	Trp	Met	Met					
		365					370					375								
tgg	tat	tgg	ggg	cca	agt	ctg	tac	aac	atc	ttg	agt	ccc	ttt	tta	cct	1204				
Trp	Tyr	Trp	Gly	Pro	Ser	Leu	Tyr	Asn	Ile	Leu	Ser	Pro	Phe	Leu	Pro					
	380					385					390									
cta	tta	cca	att	ttc	ttt	tgt	ctt	tgg	gta	tat	att	gat	tac	aag	gat	1252				
Leu	Leu	Pro	Ile	Phe	Phe	Cys	Leu	Trp	Val	Tyr	Ile	Asp	Tyr	Lys	Asp					
395					400					405					410					
gac	gac	gat	aag	ata	ccg	gtg	agc	tac	aac	ttg	ctt	gga	ttc	cta	caa	1300				
Asp	Asp	Asp	Lys	Ile	Pro	Val	Ser	Tyr	Asn	Leu	Leu	Gly	Phe	Leu	Gln					
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aga	agc	agc	aat	ttt	cag	tgt	cag	aag	ctc	ctg	tgg	caa	ttg	aat	ggg	1348				
Arg	Ser	Ser	Asn	Phe	Gln	Cys	Gln	Lys	Leu	Leu	Trp	Gln	Leu	Asn	Gly					
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Arg	Leu	Glu	Tyr	Cys	Leu	Lys	Asp	Arg	Met	Asn	Phe	Asp	Ile	Pro	Glu					
		445					450					455								
gag	att	aag	cag	ctg	cag	cag	ttc	cag	aag	gag	gac	gcc	gca	ttg	acc	1444				
Glu	Ile	Lys	Gln	Leu	Gln	Gln	Phe	Gln	Lys	Glu	Asp	Ala	Ala	Leu	Thr					
	460					465					470									
atc	tat	gag	atg	ctc	cag	aac	atc	ttt	gct	att	ttc	aga	caa	gat	tca	1492				
Ile	Tyr	Glu	Met	Leu	Gln	Asn	Ile	Phe	Ala	Ile	Phe	Arg	Gln	Asp	Ser					
475					480					485					490					
tct	agc	act	ggc	tgg	aat	gag	act	att	gtt	gag	aac	ctc	ctg	gct	aat	1540				
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Val	Tyr	His	Gln	Ile	Asn	His	Leu	Lys	Thr	Val	Leu	Glu	Glu	Lys	Leu					
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Glu	Lys	Glu	Asp	Phe	Thr	Arg	Gly	Lys	Leu	Met	Ser	Ser	Leu	His	Leu		
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aaa	aga	tat	tat	ggg	agg	att	ctg	cat	tac	ctg	aag	gcc	aag	gag	tac	1684	
Lys	Arg	Tyr	Tyr	Gly	Arg	Ile	Leu	His	Tyr	Leu	Lys	Ala	Lys	Glu	Tyr		
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agt	cac	tgt	gcc	tgg	acc	ata	gtc	aga	gtg	gaa	atc	cta	agg	aac	ttt	1732	
Ser	His	Cys	Ala	Trp	Thr	Ile	Val	Arg	Val	Glu	Ile	Leu	Arg	Asn	Phe		
		555			560					565					570		
tac	ttc	att	aac	aga	ctt	aca	ggg	tac	ctc	cga	aac	tga	gcggccgc			1779	
Tyr	Phe	Ile	Asn	Arg	Leu	Thr	Gly	Tyr	Leu	Arg	Asn						
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 <211> 582
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 18

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			20					25					30				
Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu	Asp	Pro	Ala	Phe	Gly	Ala		
		35					40					45					
Asn	Ser	Asn	Asn	Pro	Asp	Trp	Asp	Phe	Asn	Pro	Asn	Lys	Asp	Gln	Trp		
		50				55					60						
Pro	Glu	Ala	Asn	Gln	Val	Gly	Ala	Gly	Ala	Phe	Gly	Pro	Gly	Phe	Thr		
65					70				75						80		
Pro	Pro	His	Gly	Gly	Leu	Leu	Gly	Trp	Ser	Pro	Gln	Ala	Gln	Gly	Ile		
			85						90					95			
Leu	Thr	Thr	Val	Pro	Ala	Ala	Pro	Pro	Pro	Ala	Ser	Thr	Asn	Arg	Gln		
			100					105					110				
Ser	Gly	Arg	Gln	Pro	Thr	Pro	Ile	Ser	Pro	Pro	Leu	Arg	Asp	Ser	His		
		115					120					125					
Pro	Gln	Ala	Met	Gln	Trp	Asn	Ser	Thr	Thr	Phe	His	Gln	Ala	Leu	Leu		
		130				135					140						
Asp	Pro	Arg	Val	Arg	Gly	Leu	Tyr	Phe	Pro	Ala	Gly	Gly	Ser	Ser	Ser		

145 150 155 160
 Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Gly Asp
 165 170 175
 Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu
 180 185 190
 Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile
 195 200 205
 Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
 210 215 220
 Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His
 225 230 235 240
 Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys
 245 250 255
 Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile
 260 265 270
 Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro
 275 280 285
 Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys
 290 295 300
 Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr
 305 310 315 320
 Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp
 325 330 335
 Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp
 340 345 350
 Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro
 355 360 365
 Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser
 370 375 380
 Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe
 385 390 395 400

Cys Leu Trp Val Tyr Ile Asp Tyr Lys Asp Asp Asp Asp Lys Ile Pro
405 410 415

Val Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
420 425 430

Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu
435 440 445

Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
450 455 460

Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
465 470 475 480

Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
485 490 495

Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
500 505 510

His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
515 520 525

Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
530 535 540

Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
545 550 555 560

Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu
565 570 575

Thr Gly Tyr Leu Arg Asn
580

<210> 19
<211> 3359
<212> DNA
<213> Artificial Sequence

<220>
<223> HGF gene fused with HBsAg L protein

<220>
<221> CDS
<222> (23)..(3352)
<223> HGF gene fused with HBsAg L protein gene

<400> 19

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ttc	ttg	cca	ttg	gct	gct	ttg	ggt	aag	ggt	cga	caa	ggc	atg	ggg	acg			100	
Phe	Leu	Pro	Leu	Ala	Ala	Leu	Gly	Lys	Val	Arg	Gln	Gly	Met	Gly	Thr				
				15					20					25					
aat	ctt	tct	ggt	ccc	aat	cct	ctg	gga	ttc	ttt	ccc	gat	cac	cag	ttg			148	
Asn	Leu	Ser	Val	Pro	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu				
			30					35					40						
gac	cct	gcg	ttc	gga	gcc	aac	tca	aac	aat	cca	gat	tgg	gac	ttc	aac			196	
Asp	Pro	Ala	Phe	Gly	Ala	Asn	Ser	Asn	Asn	Pro	Asp	Trp	Asp	Phe	Asn				
		45					50					55							
ccc	aac	aag	gat	caa	tgg	cca	gag	gca	aat	cag	gta	gga	gcg	gga	gca			244	
Pro	Asn	Lys	Asp	Gln	Trp	Pro	Glu	Ala	Asn	Gln	Val	Gly	Ala	Gly	Ala				
	60					65					70								
ttc	ggg	cca	ggg	ttc	acc	cca	cca	cac	ggc	ggt	ctt	ttg	ggg	tgg	agc			292	
Phe	Gly	Pro	Gly	Phe	Thr	Pro	Pro	His	Gly	Gly	Leu	Leu	Gly	Trp	Ser				
	75				80				85						90				
cct	cag	gct	cag	ggc	ata	ttg	aca	aca	gtg	cca	gca	gca	cct	cct	cct			340	
Pro	Gln	Ala	Gln	Gly	Ile	Leu	Thr	Thr	Val	Pro	Ala	Ala	Pro	Pro	Pro				
				95					100					105					
gcc	tcc	acc	aat	cgg	cag	tca	gga	aga	cag	cct	act	ccc	atc	tct	cca			388	
Ala	Ser	Thr	Asn	Arg	Gln	Ser	Gly	Arg	Gln	Pro	Thr	Pro	Ile	Ser	Pro				
			110					115					120						
cct	cta	aga	gac	agt	cat	cct	cag	gcc	atg	cag	tgg	aat	tcc	aca	aca			436	
Pro	Leu	Arg	Asp	Ser	His	Pro	Gln	Ala	Met	Gln	Trp	Asn	Ser	Thr	Thr				
		125					130					135							
ttc	cac	caa	gct	ctg	cta	gat	ccc	aga	gtg	agg	ggc	cta	tat	ttt	cct			484	
Phe	His	Gln	Ala	Leu	Leu	Asp	Pro	Arg	Val	Arg	Gly	Leu	Tyr	Phe	Pro				
	140					145					150								
gct	ggt	ggc	tcc	agt	tcc	gga	aca	gta	aac	cct	ggt	ccg	act	act	gcc			532	
Ala	Gly	Gly	Ser	Ser	Ser	Gly	Thr	Val	Asn	Pro	Val	Pro	Thr	Thr	Ala				
	155				160					165					170				
tca	ccc	ata	tct	ggg	gac	cct	gca	ccg	aac	atg	gag	aac	aca	aca	tca			580	
Ser	Pro	Ile	Ser	Gly	Asp	Pro	Ala	Pro	Asn	Met	Glu	Asn	Thr	Thr	Ser				
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gga	ttc	cta	gga	ccc	ctg	ctc	gtg	tta	cag	gcg	ggg	ttt	ttc	ttg	ttg			628	
Gly	Phe	Leu	Gly	Pro	Leu	Leu	Val	Leu	Gln	Ala	Gly	Phe	Phe	Leu	Leu				
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aca	aga	atc	ctc	aca	ata	cca	cag	agt	cta	gac	tcg	tgg	tgg	act	tct			676	
Thr	Arg	Ile	Leu	Thr	Ile	Pro	Gln	Ser	Leu	Asp	Ser	Trp	Trp	Thr	Ser				
		205					210					215							
ctc	aat	ttt	cta	ggg	gga	gca	ccc	acg	tgt	cct	ggc	caa	aat	tcg	cag			724	
Leu	Asn	Phe	Leu	Gly	Gly	Ala	Pro	Thr	Cys	Pro	Gly	Gln	Asn	Ser	Gln				
	220					225					230								
tcc	cca	acc	tcc	aat	cac	tca	cca	acc	tct	tgt	cct	cca	att	tgt	cct			772	
Ser	Pro	Thr	Ser	Asn	His	Ser	Pro	Thr	Ser	Cys	Pro	Pro	Ile	Cys	Pro				
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P023P01.ST25.txt

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Gly	Tyr	Arg	Trp	Met	Cys	Leu	Arg	Arg	Phe	Ile	Ile	Phe	Leu	Phe	Ile	
				255					260					265		
ctg	ctg	cta	tgc	ctc	atc	ttc	ttg	ttg	gtt	ctt	ctg	gac	tac	caa	ggc	868
Leu	Leu	Leu	Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu	Asp	Tyr	Gln	Gly	
			270					275					280			
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Met	Leu	Pro	Val	Cys	Pro	Leu	Leu	Pro	Gly	Thr	Ser	Thr	Thr	Ser	Thr	
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ggg	cca	tgc	aag	acc	tgc	acg	att	cct	gct	caa	gga	acc	tct	atg	ttt	964
Gly	Pro	Cys	Lys	Thr	Cys	Thr	Ile	Pro	Ala	Gln	Gly	Thr	Ser	Met	Phe	
	300					305					310					
ccc	tct	tgt	tgc	tgt	aca	aaa	cct	tcg	gac	gga	aac	tgc	act	tgt	att	1012
Pro	Ser	Cys	Cys	Cys	Thr	Lys	Pro	Ser	Asp	Gly	Asn	Cys	Thr	Cys	Ile	
					320					325					330	
ccc	atc	cca	tca	tcc	tgg	gct	ttc	gca	aga	ttc	cta	tgg	gag	tgg	gcc	1060
Pro	Ile	Pro	Ser	Ser	Trp	Ala	Phe	Ala	Arg	Phe	Leu	Trp	Glu	Trp	Ala	
				335					340					345		
tca	gtc	cgt	ttc	tcc	tgg	ctc	agt	tta	cta	gtg	cca	ttt	gtt	cag	tgg	1108
Ser	Val	Arg	Phe	Ser	Trp	Leu	Ser	Leu	Leu	Val	Pro	Phe	Val	Gln	Trp	
			350					355					360			
ttc	gta	ggg	ctt	tcc	ccc	act	gtt	tgg	ctt	tca	gtt	ata	tgg	atg	atg	1156
Phe	Val	Gly	Leu	Ser	Pro	Thr	Val	Trp	Leu	Ser	Val	Ile	Trp	Met	Met	
		365					370					375				
tgg	tat	tgg	ggg	cca	agt	ctg	tac	aac	atc	ttg	agt	ccc	ttt	tta	cct	1204
Trp	Tyr	Trp	Gly	Pro	Ser	Leu	Tyr	Asn	Ile	Leu	Ser	Pro	Phe	Leu	Pro	
	380					385					390					
cta	tta	cca	att	ttc	ttt	tgt	ctt	tgg	gta	tat	att	gat	tac	aag	gat	1252
Leu	Leu	Pro	Ile	Phe	Phe	Cys	Leu	Trp	Val	Tyr	Ile	Asp	Tyr	Lys	Asp	
					400					405					410	
gac	gac	gat	aag	ata	ccg	gta	caa	agg	aaa	aga	aga	aat	aca	att	cat	1300
Asp	Asp	Asp	Lys	Ile	Pro	Val	Gln	Arg	Lys	Arg	Arg	Asn	Thr	Ile	His	
				415					420					425		
gaa	ttc	aaa	aaa	tca	gca	aag	act	acc	cta	atc	aaa	ata	gat	cca	gca	1348
Glu	Phe	Lys	Lys	Ser	Ala	Lys	Thr	Thr	Leu	Ile	Lys	Ile	Asp	Pro	Ala	
			430					435					440			
ctg	aag	ata	aaa	acc	aaa	aaa	gtg	aat	act	gca	gac	caa	tgt	gct	aat	1396
Leu	Lys	Ile	Lys	Thr	Lys	Lys	Val	Asn	Thr	Ala	Asp	Gln	Cys	Ala	Asn	
		445					450					455				
aga	tgt	act	agg	aat	aaa	gga	ctt	cca	ttc	act	tgc	aag	gct	ttt	gtt	1444
Arg	Cys	Thr	Arg	Asn	Lys	Gly	Leu	Pro	Phe	Thr	Cys	Lys	Ala	Phe	Val	
	460					465					470					
ttt	gat	aaa	gca	aga	aaa	caa	tgc	ctc	tgg	ttc	ccc	ttc	aat	agc	atg	1492
Phe	Asp	Lys	Ala	Arg	Lys	Gln	Cys	Leu	Trp	Phe	Pro	Phe	Asn	Ser	Met	
					480					485					490	
tca	agt	gga	gtg	aaa	aaa	gaa	ttt	ggc	cat	gaa	ttt	gac	ctc	tat	gaa	1540
Ser	Ser	Gly	Val	Lys	Lys	Glu	Phe	Gly	His	Glu	Phe	Asp	Leu	Tyr	Glu	

495				500				505								
aac	aaa	gac	tac	att	aga	aac	tgc	atc	att	ggc	aaa	gga	cgc	agc	tac	1588
Asn	Lys	Asp	Tyr	Ile	Arg	Asn	Cys	Ile	Ile	Gly	Lys	Gly	Arg	Ser	Tyr	
			510					515					520			
aag	gga	aca	gta	tct	atc	act	aag	agt	ggc	atc	aaa	tgt	cag	ccc	tgg	1636
Lys	Gly	Thr	Val	Ser	Ile	Thr	Lys	Ser	Gly	Ile	Lys	Cys	Gln	Pro	Trp	
		525					530					535				
agt	tcc	atg	ata	cca	cac	gaa	cac	agc	tat	cgg	ggc	aaa	gac	cta	cag	1684
Ser	Ser	Met	Ile	Pro	His	Glu	His	Ser	Tyr	Arg	Gly	Lys	Asp	Leu	Gln	
	540					545					550					
gaa	aac	tac	tgt	cga	aat	cca	cga	ggg	gaa	gaa	ggg	gga	ccc	tgg	tgt	1732
Glu	Asn	Tyr	Cys	Arg	Asn	Pro	Arg	Gly	Glu	Glu	Gly	Gly	Pro	Trp	Cys	
555					560				565						570	
ttc	aca	agc	aat	cca	gag	gta	cgc	tac	gaa	gtc	tgt	gac	att	cct	cag	1780
Phe	Thr	Ser	Asn	Pro	Glu	Val	Arg	Tyr	Glu	Val	Cys	Asp	Ile	Pro	Gln	
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tgt	tca	gaa	gtt	gaa	tgc	atg	acc	tgc	aat	ggg	gag	agt	tat	cga	ggc	1828
Cys	Ser	Glu	Val	Glu	Cys	Met	Thr	Cys	Asn	Gly	Glu	Ser	Tyr	Arg	Gly	
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ctc	atg	gat	cat	aca	gaa	tca	ggc	aag	att	tgt	cag	cgc	tgg	gat	cat	1876
Leu	Met	Asp	His	Thr	Glu	Ser	Gly	Lys	Ile	Cys	Gln	Arg	Trp	Asp	His	
		605					610					615				
cag	aca	cca	cac	cgg	cac	aaa	ttc	ttg	cct	gaa	aga	tat	ccc	gac	aag	1924
Gln	Thr	Pro	His	Arg	His	Lys	Phe	Leu	Pro	Glu	Arg	Tyr	Pro	Asp	Lys	
	620					625					630					
ggc	ttt	gat	gat	aat	tat	tgc	cgc	aat	ccc	gat	ggc	cag	ccg	agg	cca	1972
Gly	Phe	Asp	Asp	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Gln	Pro	Arg	Pro	
635					640				645						650	
tgg	tgc	tat	act	ctt	gac	cct	cac	acc	cgc	tgg	gag	tac	tgt	gca	att	2020
Trp	Cys	Tyr	Thr	Leu	Asp	Pro	His	Thr	Arg	Trp	Glu	Tyr	Cys	Ala	Ile	
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aaa	aca	tgc	gct	gac	aat	act	atg	aat	gac	act	gat	gtt	cct	ttg	gaa	2068
Lys	Thr	Cys	Ala	Asp	Asn	Thr	Met	Asn	Asp	Thr	Asp	Val	Pro	Leu	Glu	
			670					675					680			
aca	act	gaa	tgc	atc	caa	ggc	caa	gga	gaa	ggc	tac	agg	ggc	act	gtc	2116
Thr	Thr	Glu	Cys	Ile	Gln	Gly	Gln	Gly	Glu	Gly	Tyr	Arg	Gly	Thr	Val	
		685				690						695				
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Asn	Thr	Ile	Trp	Asn	Gly	Ile	Pro	Cys	Gln	Arg	Trp	Asp	Ser	Gln	Tyr	
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cct	cac	gag	cat	gac	atg	act	cct	gaa	aat	ttc	aag	tgc	aag	gac	cta	2212
Pro	His	Glu	His	Asp	Met	Thr	Pro	Glu	Asn	Phe	Lys	Cys	Lys	Asp	Leu	
715					720					725					730	
cga	gaa	aat	tac	tgc	cga	aat	cca	gat	ggg	tct	gaa	tca	ccc	tgg	tgt	2260
Arg	Glu	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Ser	Glu	Ser	Pro	Trp	Cys	
				735					740					745		
ttt	acc	act	gat	cca	aac	atc	cga	gtt	ggc	tac	tgc	tcc	caa	att	cca	2308

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Phe	Thr	Thr	Asp	Pro	Asn	Ile	Arg	Val	Gly	Tyr	Cys	Ser	Gln	Ile	Pro		
			750					755					760				
aac	tgt	gat	atg	tca	cat	gga	caa	gat	tgt	tat	cgt	ggg	aat	ggc	aaa	2356	
Asn	Cys	Asp	Met	Ser	His	Gly	Gln	Asp	Cys	Tyr	Arg	Gly	Asn	Gly	Lys		
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aat	tat	atg	ggc	aac	tta	tcc	caa	aca	aga	tct	gga	cta	aca	tgt	tca	2404	
Asn	Tyr	Met	Gly	Asn	Leu	Ser	Gln	Thr	Arg	Ser	Gly	Leu	Thr	Cys	Ser		
			780				785				790						
atg	tgg	gac	aag	aac	atg	gaa	gac	tta	cat	cgt	cat	atc	ttc	tgg	gaa	2452	
Met	Trp	Asp	Lys	Asn	Met	Glu	Asp	Leu	His	Arg	His	Ile	Phe	Trp	Glu		
					800					805					810		
cca	gat	gca	agt	aag	ctg	aat	gag	aat	tac	tgc	cga	aat	cca	gat	gat	2500	
Pro	Asp	Ala	Ser	Lys	Leu	Asn	Glu	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Asp		
				815					820					825			
gat	gct	cat	gga	ccc	tgg	tgc	tac	acg	gga	aat	cca	ctc	att	cct	tgg	2548	
Asp	Ala	His	Gly	Pro	Trp	Cys	Tyr	Thr	Gly	Asn	Pro	Leu	Ile	Pro	Trp		
			830					835					840				
gat	tat	tgc	cct	att	tct	cgt	tgt	gaa	ggt	gat	acc	aca	cct	aca	ata	2596	
Asp	Tyr	Cys	Pro	Ile	Ser	Arg	Cys	Glu	Gly	Asp	Thr	Thr	Pro	Thr	Ile		
			845				850					855					
gtc	aat	tta	gac	cat	ccc	gta	ata	tct	tgt	gcc	aaa	acg	aaa	caa	ttg	2644	
Val	Asn	Leu	Asp	His	Pro	Val	Ile	Ser	Cys	Ala	Lys	Thr	Lys	Gln	Leu		
						865					870						
cga	gtt	gta	aat	ggg	att	cca	aca	cga	aca	aac	ata	gga	tgg	atg	gtt	2692	
Arg	Val	Val	Asn	Gly	Ile	Pro	Thr	Arg	Thr	Asn	Ile	Gly	Trp	Met	Val		
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agt	ttg	aga	tac	aga	aat	aaa	cat	atc	tgc	gga	gga	tca	ttg	ata	aag	2740	
Ser	Leu	Arg	Tyr	Arg	Asn	Lys	His	Ile	Cys	Gly	Gly	Ser	Leu	Ile	Lys		
				895					900					905			
gag	agt	tgg	gtt	ctt	act	gca	cga	cag	tgt	ttc	cct	tct	cgt	gac	ttg	2788	
Glu	Ser	Trp	Val	Leu	Thr	Ala	Arg	Gln	Cys	Phe	Pro	Ser	Arg	Asp	Leu		
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Lys	Asp	Tyr	Glu	Ala	Trp	Leu	Gly	Ile	His	Asp	Val	His	Gly	Arg	Gly		
			925				930					935					
gat	gag	aaa	tgc	aaa	cag	gtt	ctc	aat	gtt	tcc	cag	ctg	gta	tat	ggc	2884	
Asp	Glu	Lys	Cys	Lys	Gln	Val	Leu	Asn	Val	Ser	Gln	Leu	Val	Tyr	Gly		
			940			945					950						
cct	gaa	gga	tca	gat	ctg	gtt	tta	atg	aag	ctt	gcc	agg	cct	gct	gtc	2932	
Pro	Glu	Gly	Ser	Asp	Leu	Val	Leu	Met	Lys	Leu	Ala	Arg	Pro	Ala	Val		
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ctg	gat	gat	ttt	gtt	agt	acg	att	gat	tta	cct	aat	tat	gga	tgc	aca	2980	
Leu	Asp	Asp	Phe	Val	Ser	Thr	Ile	Asp	Leu	Pro	Asn	Tyr	Gly	Cys	Thr		
				975					980					985			
att	cct	gaa	aag	acc	agt	tgc	agt	gtt	tat	ggc	tgg	ggc	tac	act	gga	3028	
Ile	Pro	Glu	Lys	Thr	Ser	Cys	Ser	Val	Tyr	Gly	Trp	Gly	Tyr	Thr	Gly		
			990					995					1000				

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ttg atc aac	tat gat ggc cta tta	cga gtg gca cat ctc	tat ata	3073
Leu Ile Asn	Tyr Asp Gly Leu Leu	Arg Val Ala His Leu	Tyr Ile	
1005	1010	1015		
atg gga aat	gag aaa tgc agc cag	cat cat cga ggg aag	gtg act	3118
Met Gly Asn	Glu Lys Cys Ser Gln	His His Arg Gly Lys	Val Thr	
1020	1025	1030		
ctg aat gag	tct gaa ata tgt gct	ggg gct gaa aag att	gga tca	3163
Leu Asn Glu	Ser Glu Ile Cys Ala	Gly Ala Glu Lys Ile	Gly Ser	
1035	1040	1045		
gga cca tgt	gag ggg gat tat ggt	ggc cca ctt gtt tgt	gag caa	3208
Gly Pro Cys	Glu Gly Asp Tyr Gly	Gly Pro Leu Val Cys	Glu Gln	
1050	1055	1060		
cat aaa atg	aga atg gtt ctt ggt	gtc att gtt cct ggt	cgt gga	3253
His Lys Met	Arg Met Val Leu Gly	Val Ile Val Pro Gly	Arg Gly	
1065	1070	1075		
tgt gcc att	cca aat cgt cct ggt	att ttt gtc cga gta	gca tat	3298
Cys Ala Ile	Pro Asn Arg Pro Gly	Ile Phe Val Arg Val	Ala Tyr	
1080	1085	1090		
tat gca aaa	tgg ata cac aaa att	att tta aca tat aag	gta cca	3343
Tyr Ala Lys	Trp Ile His Lys Ile	Ile Leu Thr Tyr Lys	Val Pro	
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cag tca tag	cggccgc			3359
Gln Ser				

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 <211> 1109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct
 <400> 20

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Leu Gly Lys Val	Arg Gln Gly Met	Gly Thr Asn Leu Ser	Val Pro Asn
20	25	30	
Pro Leu Gly Phe	Phe Pro Asp His	Gln Leu Asp Pro	Ala Phe Gly Ala
35	40	45	
Asn Ser Asn Asn	Pro Asp Trp Asp	Phe Asn Pro Asn	Lys Asp Gln Trp
50	55	60	
Pro Glu Ala Asn	Gln Val Gly Ala	Gly Ala Phe Gly	Pro Gly Phe Thr
65	70	75	80

Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln Ala Gln Gly Ile
85 90 95

Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser Thr Asn Arg Gln
100 105 110

Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg Asp Ser His
115 120 125

Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu
130 135 140

Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser
145 150 155 160

Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Gly Asp
165 170 175

Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu
180 185 190

Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile
195 200 205

Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
210 215 220

Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His
225 230 235 240

Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys
245 250 255

Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile
260 265 270

Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro
275 280 285

Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys
290 295 300

Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr
305 310 315 320

Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp
325 330 335

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Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp
340 345 350

Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro
355 360 365

Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser
370 375 380

Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe
385 390 395 400

Cys Leu Trp Val Tyr Ile Asp Tyr Lys Asp Asp Asp Asp Lys Ile Pro
405 410 415

Val Gln Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala
420 425 430

Lys Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys
435 440 445

Lys Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys
450 455 460

Gly Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys
465 470 475 480

Gln Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys
485 490 495

Glu Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg
500 505 510

Asn Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile
515 520 525

Thr Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His
530 535 540

Glu His Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn
545 550 555 560

Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu
565 570 575

Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu Cys
580 585 590

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Met Thr Cys₅₉₅ Asn Gly Glu Ser Tyr₆₀₀ Arg Gly Leu Met Asp₆₀₅ His Thr Glu

Ser Gly₆₁₀ Lys Ile Cys Gln Arg₆₁₅ Trp Asp His Gln Thr₆₂₀ Pro His Arg His

Lys₆₂₅ Phe Leu Pro Glu Arg₆₃₀ Tyr Pro Asp Lys Gly₆₃₅ Phe Asp Asp Asn Tyr₆₄₀

Cys Arg Asn Pro Asp₆₄₅ Gly Gln Pro Arg Pro₆₅₀ Trp Cys Tyr Thr Leu₆₅₅ Asp

Pro His Thr Arg₆₆₀ Trp Glu Tyr Cys Ala₆₆₅ Ile Lys Thr Cys Ala₆₇₀ Asp Asn

Thr Met Asn₆₇₅ Asp Thr Asp Val Pro₆₈₀ Leu Glu Thr Thr Glu₆₈₅ Cys Ile Gln

Gly Gln₆₉₀ Gly Glu Gly Tyr Arg₆₉₅ Gly Thr Val Asn Thr₇₀₀ Ile Trp Asn Gly

Ile₇₀₅ Pro Cys Gln Arg Trp₇₁₀ Asp Ser Gln Tyr Pro₇₁₅ His Glu His Asp Met₇₂₀

Thr Pro Glu Asn Phe₇₂₅ Lys Cys Lys Asp Leu₇₃₀ Arg Glu Asn Tyr Cys₇₃₅ Arg

Asn Pro Asp Gly₇₄₀ Ser Glu Ser Pro Trp₇₄₅ Cys Phe Thr Thr Asp₇₅₀ Pro Asn

Ile Arg Val₇₅₅ Gly Tyr Cys Ser Gln₇₆₀ Ile Pro Asn Cys Asp₇₆₅ Met Ser His

Gly Gln₇₇₀ Asp Cys Tyr Arg Gly₇₇₅ Asn Gly Lys Asn Tyr₇₈₀ Met Gly Asn Leu

Ser Gln Thr Arg Ser Gly₇₉₀ Leu Thr Cys Ser Met₇₉₅ Trp Asp Lys Asn Met₈₀₀

Glu Asp Leu His Arg₈₀₅ His Ile Phe Trp Glu₈₁₀ Pro Asp Ala Ser Lys₈₁₅ Leu

Asn Glu Asn Tyr₈₂₀ Cys Arg Asn Pro Asp₈₂₅ Asp Asp Ala His Gly₈₃₀ Pro Trp

Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys Pro Ile Ser

835

840

Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu Asp His Pro
850 855 860

Val Ile Ser Cys Ala Lys Thr Lys Gln Leu Arg Val Val Asn Gly Ile
865 870 875 880

Pro Thr Arg Thr Asn Ile Gly Trp Met Val Ser Leu Arg Tyr Arg Asn
885 890 895

Lys His Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp Val Leu Thr
900 905 910

Ala Arg Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr Glu Ala Trp
915 920 925

Leu Gly Ile His Asp Val His Gly Arg Gly Asp Glu Lys Cys Lys Gln
930 935 940

Val Leu Asn Val Ser Gln Leu Val Tyr Gly Pro Glu Gly Ser Asp Leu
945 950 955 960

Val Leu Met Lys Leu Ala Arg Pro Ala Val Leu Asp Asp Phe Val Ser
965 970 975

Thr Ile Asp Leu Pro Asn Tyr Gly Cys Thr Ile Pro Glu Lys Thr Ser
980 985 990

Cys Ser Val Tyr Gly Trp Gly Tyr Thr Gly Leu Ile Asn Tyr Asp Gly
995 1000 1005

Leu Leu Arg Val Ala His Leu Tyr Ile Met Gly Asn Glu Lys Cys
1010 1015 1020

Ser Gln His His Arg Gly Lys Val Thr Leu Asn Glu Ser Glu Ile
1025 1030 1035

Cys Ala Gly Ala Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp
1040 1045 1050

Tyr Gly Gly Pro Leu Val Cys Glu Gln His Lys Met Arg Met Val
1055 1060 1065

Leu Gly Val Ile Val Pro Gly Arg Gly Cys Ala Ile Pro Asn Arg
1070 1075 1080

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Pro Gly Ile Phe Val Arg Val Ala Tyr Tyr Ala Lys Trp Ile His
1085 1090 1095

Lys Ile Ile Leu Thr Tyr Lys Val Pro Gln Ser
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